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ALIGNMENTS

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erythropoietin receptor precursor - human (Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Date: 12-Feb-1993 #sequence_revision 05-Apr-1995 #text_change 22-Jun-1999 (C;Accession: A43799; A60160; A49824; A53958; A55280; I52563 R;Jones, S.S.; D'Andrea, A.D.; Haines, L.L.; Wong, G.G. Blood 76, 31-35, 1990 A;Title: Human erythropoietin receptor: cloning, expression, and biologic clark (A;Reference number: A43799; MUID:90304340 A;Accession: A43799; MUID:90304340 A;Accession: A43799

biologic characteriz

A; Molecule type: mRNA A; Residues: 1-508 < JON>

	A) RESIDUES: 1-300 COUNT
ש	A;Cross references: GB:MOU439; N1D:316Z244; FIDN:AAA3Z4U3.1; F1D:316Z243 R:Winkelmann, J.C.: Penny, I.A.: Deaven, I.L.: FORGET B.G.: Jenkins, R.B.
rinted,	Blood 76, 24-30, 1990
	A;Title: The gene for the human erythropoietin receptor: analysis of the coding seque
	A;Reference number: A60160; MUID:90304334 A;Accession: A60160
	A;Status: not compared with conceptual translation
	A; Molecule type: mRNA; DNA
on	A; Residues: 1-101, 'R', 103-188, 'RP', 191-243, 'E', 245-508 <win></win>
1 1 1 1 1	R; Noguchi, C.T.; Bae, K.S.; Chin, K.; Wada, Y.; Schechter, A.N.; Hankins, W.D.
ietin rec	Blood 78, 2548-2556, 1991
ietin rec	A; Title: Cloning of the human erythropoietin receptor gene.
ietin rec	A; Reference number: A49824; MUID:92399733
ietin rec	A; Accession: A49824
etic grow	A; Molecule type: DNA
ogene - m	A; Residues: 1-508 < NOG>
tein prec	A;Cross-references: GB:S45332; NID:g255496; PIDN:AAB23271.1; PID:g255497
tein prec	A; Experimental source: placenta
is-0 soco	A; NOTE: Sequence extracted from NCDI packbone (NCDIN:113693; NCDIE:113694)
pin recep	Exo, Hematol, 19, 973-977, 1991
pin recep	A; Title: The erythropoietin receptor gene: cloning and identification of multiple tra
receptor	A; Reference number: A53958; MUID: 91372359
pin-bindi	A;Accession: A53958
receptor	A; Molecule type: mRNA
pin recep	A; Residues: 1-508 <ehr></ehr>
pin recep	R;Penny, L.A.; Forget, B.G.
receptor	Genomics 11, 974-980, 1991
receptor	A; Title: Genomic organization of the human erythropoietin receptor gene.
in-3 rece	A; Reference number: A55280; MUID:92147143
in-9 rece	A; Accession: A55280
pin-bindi	A; Molecule type: DNA
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recentor	A. Note: the authors translated the rodon GRT for residue 31 as R
receptor	A; Note: an insert compared to other published sequences is considered by authors as 1
receptor	R; Maouche, L.; Tournamille, C.; Hattab, C.; Boffa, G.; Cartron, J.P.; Chretien, S.
2 protein	Blood 78, 2557-2563, 1991
receptor	A; Title: Cloning of the gene encoding the human erythropoietin receptor.

DB 1;

Length

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A; Cross-references: GDB:125242; OMIM:133171
A; Map position: 19p13.3-19p13.2
A; Introns: 39/1: 84/2; 143/1; 195/3; 247/1; 276/2; 305/3
A; Introns: 39/1: 84/2; 143/1; 195/3; 247/1; 276/2; 305/3
C; Superfamily: erythropoietin receptor; cytokine receptor homology
C; Keywords: alternative splicing; cytokine receptor; glycoprotein; tra:
F; 25-508/Product: erythropoietin receptor #status predicted <MAT>
F; 52-508/Product: erythropoietin receptor #status predicted <EXT>
F; 52-250/Domain: extracellular #status predicted <EXT>
F; 52-239/Domain: cytokine receptor homology CCRS>
F; 233-237/Region: WSXMS motif
F; 275-272/Domain: transmembrane #status predicted <INM>
F; 27-62,91-107/Disulfide bonds: #status predicted
F; 76/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Status: translated fro
A;Molecule type: DNA
A;Residues: 1-96 <RES>
                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-507 cMAS>
A;Cross-references: GB:D13566; NID:g286209; PIDN:BAA02761.1; PID:g286210
A;Cross-references: GB:D13566; NID:g286209; PID:g286209; 
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c; Species: Rattus norvegicus (Norway rat)
c; Species: Rattus norvegicus (Norway rat)
c; Species: Rattus norvegicus (Norway rat)
c; Accession: A46713
R; Masuda, S; Nagao, M; Takahata, K.; Konishi, Y.; Gallyas Jr.,
J. Biol. Chem. 268, 11208-11216, 1993
F;250-271/Domain: transmembrane *status predicted <TMM>F;272-507/Domain: intracellular *status predicted <INT>F;75/Binding site: carbohydrate (Asn) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Functional erythropoietin receptor of the A;Reference number: A46713; MUID:93266574 A;Accession: A46713
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C;Genetics:
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93.8%;
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Pred. No. 5.4e
11; Mismatches
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C;Accession: S14081; I49653
R;Kuramochi, S.; Ikawa, Y.; Todokoro, K.
J. Mol. Biol. 216, 567-575, 1990
A;Title: Characterization of murine erythropoletin
A;Reference number: S13249; MUID:91080149
A;Accession: S14081
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C;Keywords: cytokine receptor; transmembrane protein
F;52-238/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Lacombe, C.; Chretien, S.; Lemarchandel, V.; Mayeux, P.
J. Biol. Chem. 266, 6952-6956, 1991
A;Title: Spleen focus-forming trush long terminal repeat
A;Reference number: I49653; MUID:91201346
A;Recession: I49653
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      erythropoietin receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995
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A; Residues: 1-24 <RES>
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A; Residues: 1-265 <KUR>
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Best Local S
Matches 164
                   181 TRITIAVRARMAEPSFGGFWSAWSEPVSLLT
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TRYTFAVRARMAEPSFSGFWSAWSEPASLLT
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                                                                                                                                                                     HQAPTARGAIRFWCSLPTADTSSFVPLELRLTAASGAPRFHRVIHINEVVLLDAPVGLVA 120
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                                                                       RRAEEGSHVVLRWLPPPGAPMTTHIRYEVDVSAGNRAGGTQRVEVLEGRTECVLSNLRGG
                                                                                                                                                                                                                                                                                                            164;
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78.2%;
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Pred. No. 7.
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Pred. No. 2.
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243
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RESULT A32385

erythropoietin

receptor

precursor,

membrane-bound

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Cell 57, 277-285, 1889

A:Title: Expression cloning of the murine erythropoletin receptor.

A:Reference number: A32385; MUID:89195238

A:Accession: A32385

A:Accession: A32385

A:Accession: A32385

A:Accession: A32385

A:Coss references: GB.J04843; NID:g193090; PIDN:AAA37571.1; PID:g309219

A:Cross reference number: S13249; MUID:g1080149

A:Cross-references: EMBL:X53081; NID:g1080149

A:Cross-references: EMBL:X53081; NID:g50861; PIDN:CAA37248.1; PID:g50862

A:Cross-references: EMBL:X5308
hematopoietic growth factor receptor precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999 C;Accession: S35317; S35316 C;Accession: S35317; S35316 R;Skoda, R.C.; Seldin, D.C.; Chiang, M.K.; Peichel, C.L.; Vogt, T.F.; Leder EMBO J. 12, 2645-2653, 1993
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A:Residues: 1-507 <HIN3
A:Residues: 1-507 <HIN3
A:Cross-references: GB:S59388; NID:g237036; PIDN:AAB20029.1; I
A:Experimental source: murine erythroleukemia (MEL) cell line
R:D'Andrea, A.D.; Lodish, H.F.; Wong, G.G.
Cell 57, 277-285, 1989
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C:Date: 28-Sep-1990 #sequence_revision (05-Apr-1995 #text_change 22-Jun-1999
C:Accession: A41686; A32385; S13249
R:Hino, M.; Tojo, A.; Misawa, Y.; Morii, H.; Takaku, F.; Shibuya, M.
Mol. Cell. Biol. 11, 5527-5533, 1991
A:Title: Unregulated expression of the erythropoietin receptor gene caused by insertion A;Reference number: A41686; MUID:92017832
A;Accession: A41686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RRAEEGSHVVLRWLPPPGAPMTTHIRYEVDVSAGNRAGGTQRVEVLEGRTECVLSNLRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164;
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77.78;
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Pred. No. 1.7e-76;
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e F5-5
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18 64

PTARGAIRFWCSLPT-ADTSSFVPLELRLTAAS-GAPRFHRVIHINEVVLLDAPVGLVAR 121

SQDVFLLALGTEPLNCFSQTFEDLTCFWDEEEAA--PSGTYQLLYAYRGEKPRACPLYSQ

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RESULT
S37622
                                                                                                                                                                                                                                                                                                                                                             proto-oncogene - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S37622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane F;1-25/Domain: signal sequence #status predicted <SIG> F;26-625/Product. hematopoietic growth factor receptor #status predicted <MAT> F;26-482/Domain: extracellular #status predicted <EXT>
ρy
                                                                                                                                                                                                                                                                                                       R; Vigon, I.; Florindo, C.;
Oncogene 8, 2607-2615, 1993
A; Title: Characterization o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
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                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-626 < VIG>
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F;465-469/Region: WSXWS motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-70 <SKW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-625 <SKO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Murine c-mpl: a member of the hematopoietic growth factor receptor superfami A;Reference number: S35316; MUID:93327753 A;Accession: S35317
                                                                                                                                                      A;Cross-references: EMBL:X73677; NID:g404318; PIDN:CAA52031.1; PID:g404319
                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                               A; Accession: S37622
                                                                                                                                                                                                                                                               A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z22657
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                                                                                       Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 LADESGHVVIRW-LPPPETPMTSHIRFELDI----SAGNGAGSVQRVELLEGRT-----
                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
  4 SKAALLAARGPEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRLHQA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 SKAALLAARGPEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRLHQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVPTFGTRYVCQFPAQDEVRLFFPLHLWVKNVSLNQTLIQRVLFVDSVGLPAPPRVIKAR
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                                                                                                                                                                                                                                                                 S37622;
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                                                                   14.9%;
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                                                                                                                                                                                                                                                                                                       of the murine Mpl proto-oncogene,
                                                                                                                                                                                                                                                                                                                                                  Fichelson, S.; Guenet,
                                                                                                                                                                                                                                                                 MUID:93390934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33;
                                               Score 164; DB 2;
Pred. No. 7.6e-08;
4; Mismatches 105;
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Pred. No. 1
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.6e-08;
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RESULT
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C;Species: Homo sapiens (man)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999
C;Accession: B45266
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B45266
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A; Residues: 1-579 <VIG>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Vigon, I., Mornon, J.P.; Cocault, L.; Mitjavila, M.T. Proc. Natl. Acad. Sci. U.S.A. 89, 5640-5644, 1992 A;Title: Molecular cloning and characterization of MPL, A;Reference number: A45266; MUID:92302297
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                                                                                                                                                                                                                                         MAEPSFGGFWSAWSEPVSL 209
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                                                                                                                                                                                                                  PDGISLGGSWGSWSLPVTV
                                                                                                                                                                                                                                                               {\tt HSASALDQSPCAQPTMPWQDGPKQTSPSREASALTAEGGS-CLISGLQPGNSYWLQLRSE}
                                                                                                                                                                                                                                                                                                             GGSQPGELQISWEEPAPE--ISDFLRYELRYGPRDPKNSTGPTVIQLIATETCCPALQRP
                                                                                                                                                                                                                                                                                                                                    LADESGHVVIRW-LPPPETPMTSHIRFEL----DISAGNGAGSVQRVE--
                                                                                                                                                                                                                                                                                                                                                            SMPHFGTRYVCQFPDQEEVRLFFPLHLWVKNVFLNQTRTQRVLFVDSVGLPAPPSIIKAM
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                                                                                                                                                                                                                                                                                                                                                                                                           SQDVSLLASDSEPLKCFSRTFEDLTCFWDEEEAAPSGTYQLLYAYPRE-KP-RACPLSSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
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Pred. No. 3.
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.9e-06;
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                                                                                 homolog of
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                                                                                                         P.; Gisselbrecht,
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C;Accession: I45971
C;Accession: I45971
R;Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
A;Title: Molecular cloning of the bovine prolactin
A:Reference number: I45971; MUID:93246019
                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: cytokine receptor homology F; 36-221/Domain: cytokine receptor homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prolactin receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-581 <SCO>
                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:L02549;
                                                                                                                                                                                                                                                                                                     Best
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics
                                                                                                                                                                                                                                                                                     Matches
                                 171
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190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 GGSQPGELQISWEEPAPE--ISDFLRYELRYGPRDPKNSTGPTVIQLIATETCCPALQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122
                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                         75
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                                                                                                                                                                                                                                                7 ALLAARGPEE----LLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRLHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
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                               ECVLSNLRGRTRITIAVRARMAEPSFGGFWSAWSEPVSL
                                                                                       GLVARL---ADESGHVVIRWLPPPETPMTSH---IRFELDISAGNGAGSVQRVELLEGRT
                                                                                                                                                                                                              SLLNGQSPPEKPKLVKCRSPGKETFTCWWEPGADGGL-PTNYTLTYHKEGE----TLIHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKAALLAARGPEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRLHQA
QLKIFNLYPGQKYLVQIRCK---PDH-GYWSEWSPESSI
                                                                                                                                         CPDYKTGGPNSCYFSKKHTSIWKMYVITVNAINQMGISSSDPLY---VHVTYIVEPEPPA 131
                                                                                                                                                                           APTARGAIRFWCSLPTADTSSFVPLELRLTA-----ASGAPRFHRVIHINEVVLLDAPV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDGISLGGSWGSWSLPVTV 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAEPSFGGFWSAWSEPVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSASALDQSPCAQPTMPWQDGPKQTSPSREASALTAEGGS-CLISGLQPGNSYWLQLRSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LADESGHVVIRW-LPPPETPMTSHIRFEL----DISAGNGAGSVQRVE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQDVSLLASDSEPLKCFSRTFEDLTCFWDEEEAAPSGTYQLLYAYPRE-KP-RACPLSSQ
                                                                  NLTLELKHPEDRKPYLWIKWSPPTMTDVKSGWFIIQYEIRLKPEKATDWETHFTLKQ--T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMPHFGTRYVCQFPDQEEVRLFFPLHLWVKNVFLNQTRTQRVLFVDSVGLPAPPSIIKAM 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTARGAIREWCSLP-TADTSSFVPLELRL-TAASGAPREHRVIHINEVVLLDAPVGLVAR 121
                                                                                                                                                                                                                                                                                     l Similarity
48; Conserv
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                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                     10.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 NID:g163617;
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                                                                                                                                                                                                                                                                                     40;
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Pred. No. 4.4e-06;
Vismatches 107;
                                                                                                                                                                                                                                                                                   Score 118; DB 2
Pred. No. 0.002;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIDN:AAA51417.1;
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                                                                                                                                                                                                                                                                                                                                                                            <CRS>
                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                     101;
224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor
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                                                                                                                                                                                                                                                                                                                      Length 581;
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                                                                                                                                                                                                                                                                                     30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-Jul-2000
                                                                                                                                                                                                                                                                                     Gaps
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                                                                      189
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receptor

precursor

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somatotropin receptor - sheep

N;Alternate names: growth hormone receptor

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 08-Dec-2000

C;Accession: S33339

R;Adams, T.E.; Baker, L.; Fiddes, R.J.; Brandon, M.R.

Mol. Cell. Endocrinol. 73, 135-145, 1990

A;Title: The sheep growth hormone receptor: molecular cloning and ontogeny of mi A;Reference number: S33339; MUID:91099608

A;Accession: S33339; MUID:91099608

A;Accession: S33339; MUID:91099608

A;Accession: S33339; MUID:91099608

A;Cross-references: EMBL:M82912; NID:g165888; PIDN:AAA73171.1; PID:g165889

C;Superfamily: fibronectin type III repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999
C;Accession: B45268
R;Renauld, J.C.; Druez, C.; Kermouni, A.; Houssiau, F.; Uyttenhove, C.; Van Roost Proc. Natl. Acad. Sci. U.S.A. 89, 5690-5694, 1992
A;Title: Expression cloning of the murine and human interleukin 9 receptor cDNAs. A;Reference number: A45268; MUID:92302307
A;Accession: B45268
A;Accession: B45268
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-522 <RENY
A;Cross-references: GB:M84747; NID:9184508; PIDN:AAA58679.1; PID:9184509
C;Keywords: 91ycoprotein; receptor; T-cell proliferation; transmembrane protein
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local 53;
  170
                                          132 RWLPPPET 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 LEAFELDPGFIHEARLRVQMATLEDDVVEEERYTGQWSEWSQPV 252
                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                              NSSYTSVWTPYCIKLTSNGGIVD-HKCFSVEDIVQPDPPVGLNWTLLNISLTEIHADILV 169
                                                                                                           PTADTSSFVPLELRLTAASGAPRFHRVIHINEVVLLDAPVGLVARLADES-----GHVVI 131
                                                                                                                                                                   CRSPELETFSCHWTDGANHSLQSPGSVQMFYIRRDIQEWKEC-----PDYVSAGENSCYF 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDLQSNIS--SGHCILTWSISPALEPMTTLLSYELAFKKQEEAWEQAQHRDHIVGVTWLI
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  KWEPPPNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----CILRGSECTVVLPPEAVLVPSDNFTITFHHCMSGREQVSLVDPEYLPRRHVKLDPP
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                                                                                                                                                                                                                                                                                 Similarity
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  177
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                                                                                                                                                                                                                                                                                 10.1%;
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23.7%;
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                                                                                                                                                                                                                                                                                 Score 110.5; DB 2; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 111; DB 2;
Pred. No. 0.0086;
                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                               57;
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                                                                                                                                                                                                                                                           13;
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C;Species: Gallus gallus (chicken)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995
C;Accession: S32823; A49812
C;Superfamily: fibronectin type III repeat homology C;Superfamily: fibronectin type III repeat homology C;Keywords: alternative splicing; receptor; sex-linked inheritance; transmembrane F;1-22/Domain: signal sequence #status predicted <SIG> F;23-109/Product: somatotropin receptor, short form #status predicted <SHO>
                                                                                                                                   A;Cross-references: GB:S68576; NID:g499137; PIDN:AAB29983.1; PID:g499138
A;Experimental source: liver, normal chicken
A;Note: this truncated form is a minor splice form in normal chickens and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:M74057; NID:g211810; PIDN:AAA48781.1; PID:g211811 R;Huang, N.; Cogburn, L.A.; Agarwal, S.K.; Marks, H.L.; Burnside, J. Mol. Endocrinol. 7, 1391-1398, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Burnside, J.; Liou, S.S.; Cogburn, L.A.
Endocrinology 128, 3183-3192, 1991
A;Title: Wolecular cloning of the chicken growth
A;Reference number: S32823; MUID:91243665
                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-109 <HUA>
                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Overexpression of a truncated growth A; Reference number: A49812; MUID:94158898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-608 <BUR>
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                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                    A; Accession: A49812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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Matches
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                                    179
193
                                                                    137 GIHGDIQVRWDPPPTADVQKGWITLEYELQYKEVNET----KWKELEPRLSTVVPLYSLK 192
                                                                                                        127
                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                             69 AIRFWCSLPTADTSSFVPLELRLTAASGAPRFHRVIHINEVVLLDAPVGLVARLADES--
                                                                                                                                                                                                                                                      14 PEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQL-----EDEPWKLCRLHQAPTARG
                                  GRTRITIAVRARM-AEPSFGGF
                                                                                           ---GHVVIRWLPPPETPMTS---HIRFELDISAGNGAGSVQRVELLEGRTECV--LSNLR 178
MGRDYEIRVRSRQRTSEKFGEF
                                                                                                                                           AGENSCYFNTSYTSIWIPYCVKL-ANKDEVFDEKCFSVDEIVLPDPPVHLNWTLLNTSQT 136
                                                                                                                                                                                                                 PQISKCRSPELETFSCYWTD-----GKVTTSGTIQLLYMKRSDEDWKEC-----PDYIT
                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                         9.7%;
                                                                                                                                                                                                                                                                                          26;
                                  199
                                                                                                                                                                                                                                                                                      Score 107; DB 2
Pred. No. 0.025;
6; Mismatches
                                                                                                                                                                                                                                                                                                                            2
                                                                                                                                                                                                                                                                                                                            Length 608
                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                      89
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AG AG

DP GA

밁

В

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prolactin receptor 2 precursor - rabbit
N;Alternate names: prolactin receptor, mammary gland
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Jul-2000
C;Accession: A30304; A60380
                                                                                              A; Molecule type: mRNA
A; Residues: 1-616 <EDE>
A; Cross-references: GB:J04510;
                                                                                                                                                                                                                                                   R; Edery, M.; Jolicoeur, C.; Levi-Meyruels, C.; Dusanter-Fourt, Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989
                                                                                                                                                                            A; Reference number: A; Accession: A30304
                                                                                                                                                                                                      A; Title: Identification and sequence analysis of a second A; Reference number: A30304; MUID:89184578
                       A; Title: Purification and
                                                                      R; Waters, M.J.; Spencer, S.A.
                                               J. Biochem.
                                               22, 1089-1095,
A60380; MUID:91146782
                                                                      Hamlin, G.;
                                                                           NID:g165669; PIDN:AAAA31457.1; PID:g165670 Hamlin, G.; Henzel, W.J.; Wood, W.I.
                                                    1990
                          of the
                                                                         Henzel,
                          rabbit
                                                                         ₩.J.;
                    mammary gland
                                                                                                                                                                                                                              form
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                       prolactin
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A;Accession: A60380
A;Accession: A60380
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 41-58, X',60-66;90-93,'X',95-96,'X',98-103,'X',105,'NX',108;150-164,'XX',167
A;Residues: 41-58, X',60-66;90-93,'X',95-96,'X',98-103,'X',105,'NX',108;150-164,'XX',167
A;Residues: 41-58, X',60-66;90-93,'X',98-103,'X',105,'NX',108;150-164,'XX',167
A;Residues: 41-58, X',98-103,'X',98-103,'X',105,'NX',108;150-164,'XX',167
A;Residues: 41-58, X',98-103,'X',98-103,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X',105,'X'
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:M31680; NID:g193506; PIDN:AAA37689.1; PID:g309252 C;Superfamily: fibronectin type III repeat homology C;Keywords: glycoprotein; receptor: transmembrane protein F:1-18/Domain: signal sequence #status predicted <SIG> F:19-677/Product: somatotropin-binding protein, high molecular weight #status F:274-297/Domain: transmembrane #status predicted <TMM> F:274-297/Domain: transmembrane #status predicted <TMM> F:40,164,169/Binding site: carbohydrate (Asn) (covalent) #status predicted F:164,169/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         somatotropin-binding protein, high molecular weight, precursor - m XAlternate names: growth hormone-binding protein, high molecular C:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 08
C:Accession: S33608; S33607
C:Accession: S33608; S33607; Falamantes, F.
Mol. Endocrinol 3, 984-990, 1989
A:Title: Mouse serum growth hormone (GH) binding protein has GH re
A:Reference number: S33607; MUID:89295449
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                                                                                                                                                                                              δÃ
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A; Molecule type: mRNA
A; Residues: 1-324 <SM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:M33324; NID:g193508; PIDN:AAA37690.1; A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-677 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S33608
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 VLSNLRGRTRITIAVRARMAEPSFGGFWSAWSEPVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 TLEVKHPEDRKPYLWVKWLPPTLVDVRSGWLTLQYEIRLKPEKAA--EWETHFAGQQTQF 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 ---VARLADESGHVVIRWLPPPETPMTS---HIRFELDISAGNGAGSVQRVELLEGRTEC 172
                                                                                                                     51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 KAALLAARGPEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRLHQAP
                                                                                                                                                                                  PEELLCFTERLEDLVCFFEEAASAGV-GPGNFSFSFQLED---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYKTGGPNSCYFSKKHTSIWTIYIITVNATNQMGSSVSDPRY---VDVTYIVEPDPPVNL
LHQAPTARGAIRFWCSLPTADTSSFVPLELRLTAASGAPRFHRVIHINEVVLLDAPVGLV 119
                                                                                                             PRFTKCRSPELETFSCYWTEGDNPDLKTPGSIQLYYAKRESQRQAARIAHEWTQEWKEC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPFIFKCRSPEK-----ETFTCWWRPGADGGL-PTNYTLTYHKEGE----TITHECP
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                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                       Score 103.5; DB Pred. No. 0.063; 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 104; DB 2; Pred. No. 0.05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100;
                                                                                                                                                                                                                                                                               89;
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                                                                                                                                                                                                                                                                               47;
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                                                                                                                                                                                                                                                                               10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           predicted
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C; Accession: JQ1655
R; Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A; Title: Double antenna structure of chicken prolactin
A; Reference number: JQ1655; MUID:93075121
                                     QY
                                                                                    Вb
                                                                                                                              Q
                                                                                                                                                                           В
                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                    Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;239-425/Domain: cytokine receptor homology <CRS2>F;439-462/Domain: transmembrane #status predicted <TMM>F;59,91,100,112,132,262,303,315,335,647,701,800/Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prolactin receptor precursor - chicken
C; Species: Gallus gallus (chicken)
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δã
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뮹
                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1-23/Domain: signal sequence #status predicted <SIG>F;24-831/Product: prolactin receptor #status predicted F;36-219/Domain: cytokine receptor homology <CRS1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: cytokine receptor homology
C;Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-831 <TAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: JQ1655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: DDBJ:D13154; NID:g222848; PIDN:BAA02439.1; PID:g222849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JQ1655
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Best Local :
                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                119 VARL---ADESGHVVIRWLPPPETPMTS-HIRFELDISAGNGAGSVQRVELLEGRTECVL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170
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397 FSLNPGKKYIIQIHCK---PDHHGSWSEWS
                                            175 SNLRGRTRITIAVRARMAEPSFGGFWSAWS
                                                                                                                                                                             280 DYRTAGPNSCYFDKKHTSFWTIYNITVRATNEMGSNSSDPHY---VDVTYIVQPDPPVNV
                                                                                                                                                                                                                                                                      233 KPTIIKCRSPEK-----ETFTCWWKPGLDGG-HPTNYTLLYSKEGEE----QVYECP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 GPIWLTYCPVYSLRMDKEHEVRVRSR--QRSFEKY-SEFSEVLRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 ARLADES----
                                                                                                                                                                                                                         65 TARGAIRFWCSLPTADTSSFVPLELRLTAA-----SGAPRFHRVIHINEVVLLDAPVGL 118
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                5 KAALLAARGPEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRLHQAP
                                                                                      TLELKKPINRKPYLVLTWSPPPLADVRSGWLTLEYELRLKPEEGEEWETIFVGQQTQYKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----TECVLSNLRGRTRITIAVRARMAEPSFGGFWSAWSEPVSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WTLLNISLTGIRGDIQVSWQPPPNADVLKGWIILEYEI------QYKEVNESKWKVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----PDYVSAGKNSCYFNSSYTSIWIPYCIKLT-TNGDLLDQKCFTVDEIVQPDPPIGLN 164
                                                                                                                                                                                                                                                                                                                                                             42;
                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GHVVIRWLPPPETP-MTSHIRFELDISAGNGAGSVQRVELLEGR----
                                                                                                                                                                                                                                                                                                                                                                               9.4%;
                                                                                                                                                                                                                                                                                                                                                          37;
                                                                                                                                                                                                                                                                                                                                                                             Score 103.5; DB Pred. No. 0.082;
                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                            204
  423
                                                                                                                                                                                                                                                                                                                                                             102;
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